Appendix C

TMDL Analysis for Pathogens for Yellow Creek and Little Yellow Creek Watersheds

Pathogen TMDL Development

A TMDL is a tool for implementing water quality standards, and is based on the relationship between pollution sources and in-stream water quality conditions. TMDLs establish allowable loadings or other quantifiable parameters for a waterbody, and thereby provide the basis for states to establish water quality-based controls. These controls should provide the pollution reduction necessary for a waterbody to meet water quality standards.

A TMDL is defined as the sum of its load allocations, wasteload allocations and a margin of safety. Load allocations (LA) are the portion of the TMDL reserved for nonpoint sources of pollution. Wasteload allocations are the portion reserved for point sources. The margin of safety (MOS) is a portion of the TMDL reserved for uncertainty in the method of calculation. MOS may be included explicitly or implicitly. TMDLs are required to consider both critical conditions and seasonality for each parameter of concern.

TMDLs may be expressed in terms of either mass per time, toxicity or other appropriate measures. Additionally, TMDLs may be developed at variable temporal and spatial resolutions. The acronym TMDL implies that the maximum load is expressed in days; however, TMDLs are often calculated on a monthly, seasonal, or annual basis dependent upon the nature of the parameter of concern. The spatial scale at which a TMDL is calculated is dependent upon the distribution of impairment within the TMDL study area. TMDLs can be calculated for individual stream segments, subwatersheds or entire watersheds.

TMDL development requires the definition of the existing load, calculation of the loading capacity and allocation of the TMDL. The existing load is the quantity of a pollutant that, prior to TMDL implementation, is contributed to a waterbody. The existing load includes contributions from all sources, including point, non-point, and natural. The loading capacity is the quantity of a pollutant that a waterbody can receive and still maintain water quality standards. The loading capacity is dependent upon the physical, chemical and biological processes occurring in the waterbody. Allocation of the TMDL involves the equitable distribution of the loading capacity to all known sources in consideration of technical and economic feasibility, as well as water-quality related implications.

Methods of Pathogen TMDL development

This section outlines the TMDL methods that are used to address each cause of recreational water quality impairment. Pathogens are regulated in waters of the state (excluding the Ohio River) during the recreational season of May 1 to October 15. In the Yellow Creek Basin, the pathogen TMDL was developed for significantly impaired HUC 14 areas. The USEPA Bacteria Indicator Tool (BIT) build up and washoff model was utilized for gross coliform discharges to the HUC units. Data from the US Department of Agriculture, US Census Bureau, the NRCS, and the local county health departments was applied to the BIT model input. Output results of gross coliform loading were coupled with the SCS curve number storm water runoff hydrology method and USGS gage baseflow separation to determine in-stream concentrations. Therefore, pathogen TMDL development was created for the recreational season only.

Hydrology method SCS Curve Number Method

Daily runoff volumes for ten recreational seasons are calculated using the Natural Resources Conservation Service's Runoff Curve Number method (SCS, 1986). This method determines the amount of precipitation that flows off the surface and is adjusted for antecedent soil moisture before the precipitation event, growing or dormant season, detention potential, and soil characteristics. Curve numbers vary by land cover, use and soil type; the higher the curve number the more runoff produced. The predicted surface runoff flow is the quick response flow including interflow and drainage from tiles.

The model is applied for each pathogen impaired watershed using Theissen area weighted precipitation data from Midwest Regional Climatic Center (MRCC) weather stations that are applicable to the respective watershed. A ten year record of weather data from the MRCC stations named Millport_2_NW (#335315), Steubenville (#338025), Hopedale (#333838), and Prospect (#336861) were used as input. Table C1 provides the areas (areas and percent of total watershed) for each modeled HUC 14 watershed within the Theissen polygon for the respective MRCC station. Figure C1 indicates the pathogen modeled HUC 14 drainage areas (shaded in red) as well as the weather station Theissen polygons. The average temperature of the daily average temperature readings were used as well as a weighted average rainfall utilizing the Theissen polygon method.

To simplify the modeled drainage network, a schematic (Figure C2) was created. Shown in the red boxed areas are the pathogen impaired HUC 14 modeled watersheds. It is important to note that three unsewered communities (Amsterdam, Bergholz, and Irondale) were all located within the pathogen TMDL watersheds.

Table C1. HUC 14 area within Thiessen Polygon for each MRCC Station

HUC_14	HUC 14 area within Thiessen Polygon for each MRCC Station							
	#333838		#338025		#335315		#336861	
	(Acre)	(% Total)	(Acre)	(% Total)	(Acre)	(% Total)	(Acre)	(% Total)
5030101-180-010	20502	71.17%	0	0.00%	0	0.00%	1.7	0.02%
5030101-180-020	0	0.00%	0	0.00%	11214.4	29.61%	7653.2	99.98%
5030101-180-040	8305.9	28.83%	3652.2	68.85%	9903.9	26.15%	0	0.00%
5030101-190-040	0	0.00%	1652.5	31.15%	16756.5	44.24%	0	0.00%

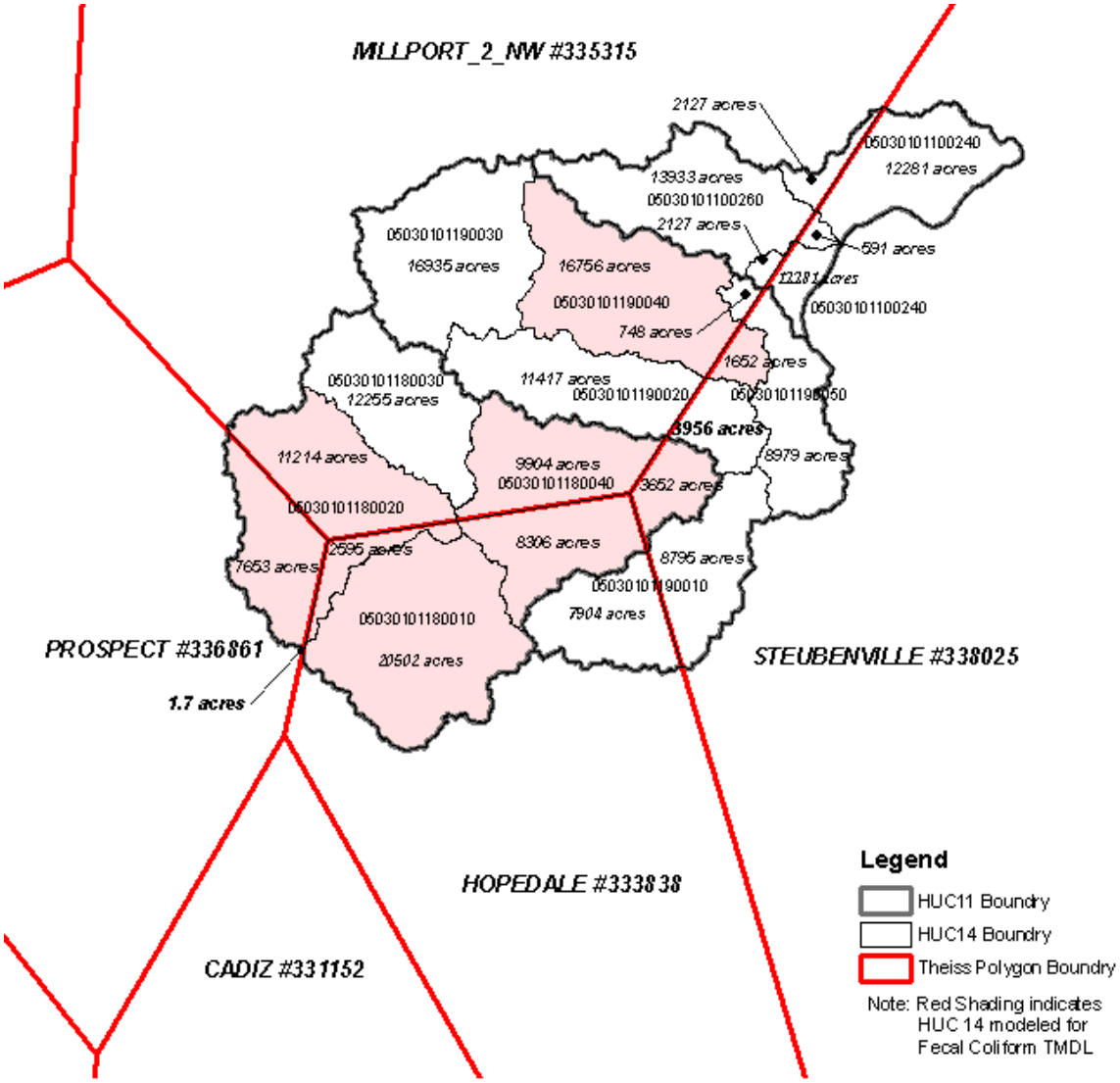

Figure C1. Yellow Creek HUC 14 watersheds modeled for pathogen TMDL determination

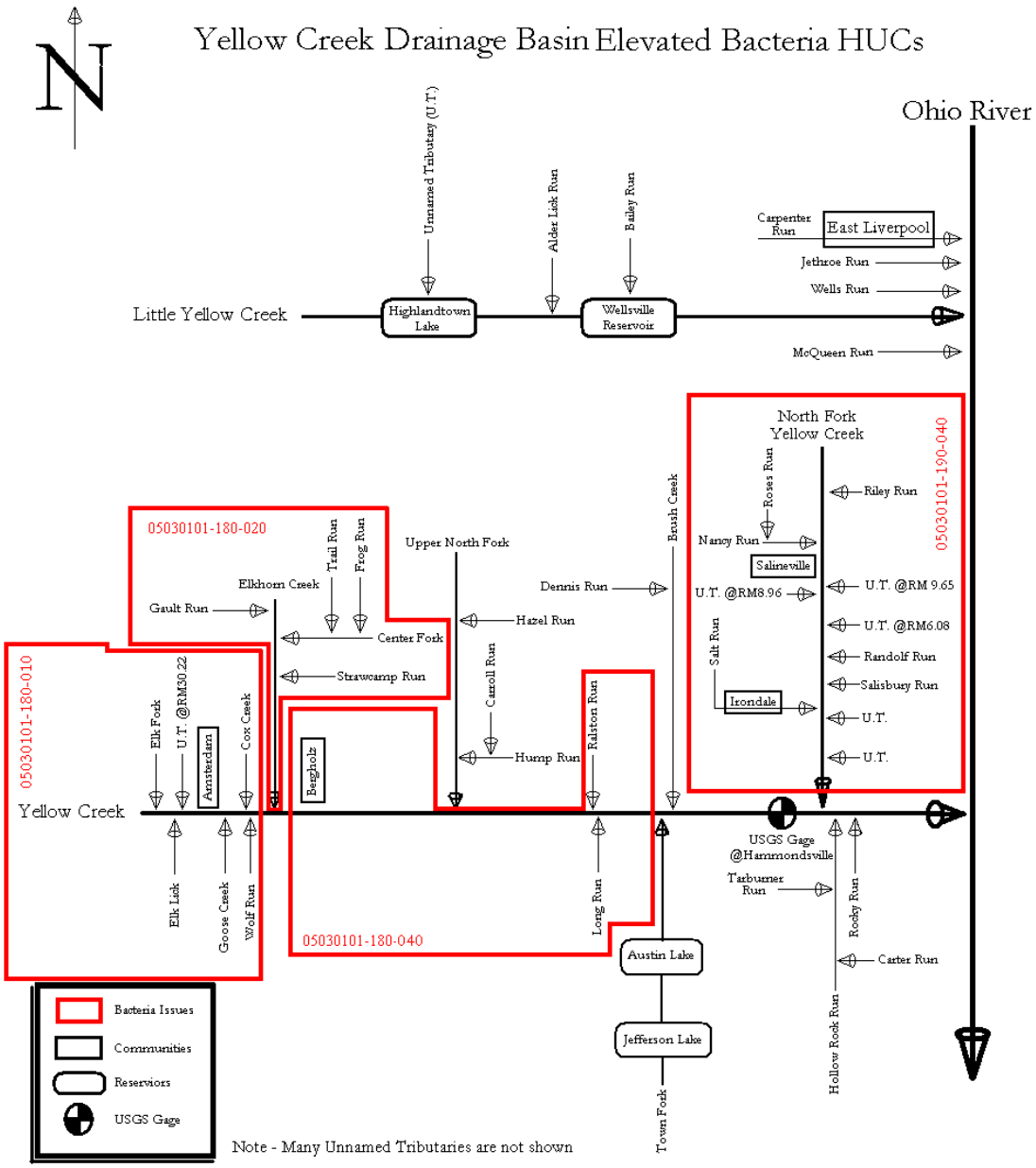

Figure C2. Schematic of Yellow Creek emphasizing areas modeled for pathogen TMDL

Land Use

Land use, soil and weather data are critical components of hydrology functions of GWLF. The National Land Cover Dataset (NLCD) is used as the land cover resource for this study. NLCD is compiled from Landsat TM satellite imagery circa 1992 and includes 23 classes of land use (USGS, 2000).

Geographical Information System (GIS) data is used to determine soil properties. GIS data indicate tabular and spatial components. Soil GIS tabular or attributes data includes

properties such as soil erodibility and slope. Spatial aspects indicate precisely where certain map units, which the tabular data relate to, exist. The Natural Resource Conservation Service's State Soil Geographic (STATSGO) and Soil Survey Geographic Database (SSURGO) databases are used to obtain all needed soils information. STATSGO is a generalized GIS database of soil parameters originally produced from more detailed soil survey data. The mapping scale for STATSGO is 1:250,000. Table C2 provides the area weighted curve numbers (CN) and area in acres for each land use within the pathogen modeled HUC 14 watersheds. As the table indicates, the predominantly land use within these watersheds is forest with the largest remainder being pasture. Very small portions of the watershed were urbanized. In addition, the watersheds were very similar in total size.

Table C2. Yellow Creek pathogen modeled watershed HUC 14 SCS curve numbers and area

	05030101-180-010		05030101-180-020		05030101-180-040		05030101-190-040	
Land Use	CN (unitless)	Area (acres)	CN (unitless)	Area (acres)	CN (unitless)	Area (acres)	CN (unitless)	Area (acres)
Cropland	82.6	987.5	82.3	1754.0	82.8	1393.9	82.9	1211.5
Forest	68.5	13029.2	67.3	13743.2	74.2	16433.8	73.9	13907.4
Urban Greenspace	0.0	0.0	73.4	180.2	0.0	0.0	79.9	38.6
Pasture	74.0	6022.1	73.7	5600.3	79.3	3414.3	78.5	2858.1
Urban	89.2	302.4	88.9	50.0	91.2	150.4	91.1	179.7
Water	100.0	104.3	100.0	63.8	100.0	312.6	100.0	134.6
Wetland	100.0	31.8	100.0	47.1	100.0	132.8	100.0	57.8
Total		20477.2		21438.6		21837.8		18387.7

The Bacteria Indicator Tool method

All the watersheds within the Yellow creek basin were sampled for fecal coliform bacteria during the summer of 2005. Results of this sampling effort were reviewed and basins which had exceedances of bacteria standards (recreataional use) were determined as summarized in Table C3. The HUC 14 units determined to be modeled for pathogen impairment were found by review of the significance of the number of samples in exceedance coupled with the proportion of sites within the HUC 14 that had exceedances. If a HUC unit had numerous sampling locations with multiple samples that exceeded recreational use standards, the entire 14-digit HUC is modeled. All recreational use impaired watersheds are modeled by BIT.

Table C3. Summary of pathogen TMDL development

Development step	Source	Method
Existing load	Surface runoff	BIT tool with spreadsheet runoff model
	Point source	No Point Source Discharges within the Impaired HUC Units
	HSTS	Population served by failing HSTS estimated via GIS and county Health Departments. Fecal coliform load based upon population census and growth/decline estimates and BIT Model per capita loading rate
Calculation of loading capacity	-	Product of the recreation season discharge volume from each sub-basin (SCS CN hydrology and USGS gage Base flow separation) and the allowable fecal coliform geometric mean concentration
Allocation	Point sources	Village of Salineville NPDES permit limit allocated
	Surface runoff	Total Allowable Load Allocation is equal to the sum of all WLAs subtracted from the assimilative capacity.
	HSTS	Septic systems are allocated a bacteria concentration and subsequent load in compliance with Individual HSTS NPDES permit

Existing loads

The U.S. EPA's Bacteria Indicator Tool (BIT) is employed to estimate the fecal coliform load accumulated within the watershed in each 14-digit HUC or tributary determined to be recreationally impaired. BIT estimates the monthly accumulation rate of fecal coliform bacteria on four land uses (cropland, forested, built-up, and pastureland), as well as the asymptotic limit for that accumulation should no washoff occur. It also

estimates the direct input of fecal coliform bacteria to streams from grazing agricultural animals and failing HSTSs (USEPA, 2000). No hydrologic or contaminant routing was considered in this model application. All bacteria loading reaching waters of the state is assumed to be completely mixed within the entire flow of the stream network being modeled.

BIT utilizes user-defined, default and literature values for various needed parameters. These parameters characterize the watershed and activities that occur within the watershed. User-defined values are required to be specific to the study area. These values include land use distribution, number and types of agricultural animals as well as wildlife densities. Default values are supplied by the tool; however, where information was available, the values were modified to reflect the study area characteristics more realistically.

Default values which were used in the Yellow Creek BIT simulation include the fraction of manure applied to each land use for each month, the fraction of manure type that is incorporated into the soil during land application, and the time spent grazing or confined by agricultural animals. Like default values, literature values are supplied by the tool; however, they may be replaced with user values if more accurate information is available for the study area. Literature values required by the tool are common to all drainage areas and include animal waste production rates and fecal coliform bacteria content as well as residential sewage discharge rates and raw sewage fecal coliform bacteria content. From the mass and concentration of bacteria from agricultural and wildlife animals, fecal coliform bacteria accumulation rates for each land use are determined by BIT.

Literature values are unchanged for each HUC because no watershed-specific information on these characteristics is available to better characterize the watershed in the relevant aspects. The amount of time cattle has accessible to streams during grazing was considered to be 100%. This was determined by observation of streams in fenced grazing areas during field visits to the drainage basin. All other default values are left unchanged. User-defined values are determined via the following methods:

• The land use distribution is derived from the National Land Cover Dataset (NLCD) via GIS analysis. The NLCD is compiled from Landsat ™ satellite imagery between 1991 and 1993 (USGS, 2000). NLCD information was manually reclassified to agree with the land use categories of BIT.

• Populations of agricultural livestock and wildlife are derived from countywide figures. Information regarding the amount of livestock is obtained from Ohio Agricultural Statistics Service published data. Information regarding wildlife populations is obtained from Ohio Department of Natural Resource census data. In each case, the total number of animals within the county is divided by the total number of acres of relevant land use in the county. The resulting animal densities (animals per acre) are used to estimate the animal populations within each 14-digit HUC.

After the wastershed charateristics are entered, BIT predicts the maximum surface accumulation rate of fecal coliform and the asymptotic limit of accumulation should no washoff occur. Additionally, BIT predicts the fecal coliform load contributed directly to the stream from livestock with stream access as well as home septic system discharge load.

To complement BIT, a spreadsheet method was developed used to estimate the pollutant loads from bacteria washoff utilizing hydrology calculations from the SCS curve-number method. To appropriately determine the hydrology using the SCS method, hydrologic response units were developed by overlying the NLCD land use with State Soil Geographic (STATSGO) Database from the Natural Resources Conservation Service - National Cartography and Geospatial Center. Utilizing GIS raster math, special areas for each land use with each soil type combination was determined. With the combined data set, the SCS curve-number method was employed for each of these areas within each modeled HUC 14 unit. These methods use a combination of known land use data and empirically derived runoff functions in each calculation. The SCS method was followed utilizing an initial abstraction of 20% of total storage.

Bacteria washoff is estimated using the daily land-surface accumulation rate generated by BIT, and a washoff equation common to SWMM, HSPF and GWLF. This equation assumes the percent washoff is proportioned to the rainfall amount produced within one day. The proportion exponentially increases with rainfall depth and the rate of increase is considered to be greater in urban areas than non-urban areas.

Urban area $$\%washoff = 1 - e^{\frac{\ln 0.1}{0.5}Q}$$

Non-urban area $$\%washoff = 1 - e^{\frac{\ln 0.1}{0.65}Q}$$

Where Q is the rainfall runoff (inches) per unit area of land surface from the SCS curve-number method. In addition to the daily accumulation rate, the washoff equation requires daily runoff and a washoff coefficient as inputs. Daily runoff is estimated using the SCS curve-number method.

Within the HUC 14 units modeled for bacteria impairment, are defined as primary contact recreational use as defined in OAC rule 3745-1-07. There was one NPDES point source discharger within the modeled area. The Village of Salineville (3PB00026) discharges to the North Fork of Yellow Creek within HUC 05030101-190-040. No increase in design flow for this POTW is expected in the near future. Therefore, the facility's permitted design flow and the fecal coliform geometric mean standard of 1000 cfu per 100 mL are used for future as well as existing load calculations.

The number of HSTS and the percentage of those which are failing are determined via GIS analysis and discussion with the local health department officials, respectively. The

number of HSTS in each 14-digit HUC is estimated based upon 1990 and 2000 census demographic information and projection of population change by the Ohio Department of Development. HSTS pollutant loads are estimated as the product of the number of persons served by failing systems in each subwatershed by a per capita wastewater flow-rate and representative wastewater-quality information. BIT provides referenced default rates for each of these input parameters.

Bacteria loadings are difficult to accurately quantify because because of the difficulty to obtain adequate data to accurately characterize the highly variable individual sources. In addition, many factors affect bacteria which are difficult to model. Metorological conditions, pathogens' life cycle characteristics and waste placement in relation to the stream network are dynamic and highly variable parameters which must be simulated by modeling. In such situations, BIT provides a means to make estimations of bacteria loads based upon empirical studies in other watersheds. While the use of such literature and default values results in considerable uncertainty, it is the best option available considering time and resource limitations. The literature and default values used in the load calculations are best professional judgment representations of the actual watershed conditions. Where applicable, the actual watershed characteristics were utilized in BIT input.

One additional source of error in BIT input could exist in animal population distribution. Animal population statistics information from the United States Department of Agricultural are assumed to be evenly distributed throughout the HUC 14 on a countywide basis. This is a broad assumption which could lead to error because often the animals are often clustered on farms which are not always evenly disbursed throughout a county. Completing error analysis of these assumptions is beyond the scope of this study.

Home Sewage Treatment Systems

The number of HSTS and the percentage of those which are failing is determined via GIS analysis. The number of HSTS in each 14-digit HUC is estimated based upon 1990 and 2000 census demographic information, except for Coshocton County. The Coshocton County Health Department provided their own GIS data of the distribution of HSTS. The percentage of failing HSTS is based on information from health departments, field observations and GIS analysis of the age of houses in a watershed.

HSTS pollutant loads are estimated as the product of the number of persons served by failing systems in each subwatershed, a per capita wastewater flow-rate and representative wastewater-quality information. BIT referenced values of sewage production rates from domiciles and quality of that waste was utilized in the modeling effort. The fecal coliform concentration reaching the stream from failing HSTS is assumed to average $1.00*10^8$ colony forming units per 100 mL and the average failing septic flow rate is 70 gal per person per day.

Table C4. Home sewage treatment systems estimated values for Yellow Creek Watershed

Subwatershed	Total Area (acres)	Failing Septics (#)	Total Persons Served (#)	Septic Flow to Stream (gal/day)	Fecal Coliform Loading (count/day)
05030101-180-010	20379.3	655	1720	120391	4.56E+14
05030101-180-020	21352.9	560	1398	97878	3.70E+14
05030101-180-040	21510.3	524	1382	96754	3.66E+14
05030101-190-040	18222.2	604	1700	118978	4.50E+14

Upstream Dilution

Four 14-digit HUC watersheds were analyzed for bacteria impairment. Because the entire HUC 14 areas were modeled, all runoff in the watersheds was included for bacteria runoff. No upstream flow existed for bacteria modeling efforts.

Baseflow was determined for each HUC 14 unit modeled by proportioning yield within the Yellow Creek watershed. Baseflow separation utilizing CleLand's method of the Hammondsville USGS gage drainage was completed for the previous ten year record. Runoff yields were also developed for each year to utilize in the BATHTUB portion of this TMDL. The baseflow was determined for each HUC 14 modeled by proportioning the spatial area of the HUC to the gage drainage. These yields were utilized on a daily basis along with the SCS runoff curve number method incorporating Thiess polygon proportioned precipitation data to develop total dilution for daily pathogen loading at each HUC 14 outlet. These groundwater and runoff flows were used for loading assimilative capacity analysis and subsequent allocation for pollutant sources.

Loading capacity and TMDL

Seasonal loading capacity for each HUC 14 watershed is determined by calculating the product of the seasonal stream flow and fecal coliform geometric mean concentration target for ten previous years. The seasonal base flow of each HUC 14 was determined by developing a baseflow by CleLand's baseflow separation technique for ten years of the recreational season (May 1 to October 15) hydrologic record. This baseflow was proportioned to each HUC 14 by area. Runoff flows were developed for each HUC 14 by the SCS curve-number method incorporating GIS land use data. The geometric fecal coliform mean target of 1000 cfu per 100 mL for each of the HUC 14 molded areas (all primary recreational use streams) was used as the assimilative capacity. The loading

capacity calculation assumes uniform, steady state physical dilution as a means of assimilation. No in-stream bioprocesses nor flow routing is attempted in this model procedure for pathogens.

Allocations
Existing modeled fecal coliform loads are allocated for each watershed to meet the seasonal TMDL. To complete allocations, the portions of bacteria sources which could not be altered readily were initially issued fractions of the assimilative capacity. Therefore, pathogen indicator loading from the land uses of forest, green space, water bodies, and wetlands were issued full allocations because it is not considered practicable to reduced these unmanaged land use sources. In addition, because the Village of Salineville currently discharges under an NPDES permit, the permitted maximum fecal coliform (equal to the geometric mean fecal coliform standard) was allocated to this discharger.

Conversly, HSTSs are point sources from which no wasteload is expected if elimination of failing systems is completed. Therefore, the HSTS were viewed as needing 100 percent reduction. However, in some HUC 14s modeled, if elimination of this source were completed, large assimilative capacity would be freed creating large margins of safety. Allocations were given to HSTS in HUC 14s where a smaller than 100 percent reduction was needed to meet the assimilative capacity with five percent margin of safety. This allocation is not permitting the failing HSTS source load, but allows for practicable removal with the expectation that the 100 percent removal rate will be accomplished within all the HUC 14s modeled.

Fecal coliform from cows grazing in streams are also allocated. The practice of allowing livestock access to the stream hinders water quality; however, when the entire HUC 14 was model, the current level of bacteria from direct animal input was typically not considered to be significant. Hoewever, livestock accessing the stream can create unsanitary conditions within the near reaches of the receiving stream. This issue is not addressed in this TMDL because the modeling was completed on a basin wide scale. Only within HUC 50030101-190-040 was a percent reduction of direct animal input of pathogens required for the stream to meet assimilative capacity. The direct animal input pathogens were allocated after failing HSTS. The order of allocation was chosen because failing HSTS are more readily eliminated as a pathogen source than livestock in streams. No other percent reductions were required for any of the HUC 14s modeled.

Critical condition and seasonality

The critical condition for pathogens is the summer dry period when flows are lowest, and thus the potential for dilution is the lowest. Summer is also the period when the probability of recreational contact is the highest. For these reasons recreational use designations are only applicable in the period May 1 to October 15. Pathogen TMDLs are developed for the same May to October 15 time-period in consideration of the critical condition, and for agreement with Ohio WQS. With regard to pathogens, the TMDL and allocations were completed for this recreational season only.

Margin of Safety

Margin of safety (MOS) is a required component of TMDLs in order to account for the uncertainty concerning the relationship between pollutant loads and of the quality of receiving waterbodies. The MOS can be incorporated implicitly by the conservative assumptions in the development of TMDLs. They can also be incorporated explicitly by quantitatively allocating a portion of the loading capacity specifically for the MOS. For the pathogen TMDL, a five percent explicit margin of safety was provided in the allocations.

Model Results

Results of BIT coupled with the SCS curve number method for hydrology modeling for the four HUC 14s appeared to be reasonable. Figures C3, C4, C5, and C6 present fecal coliform modeling results for HUC 50300101-180-010, 50300101-180-020, 50300101-180-040, and 50300101,190-040. Bacteria is represented as concentration of coliny forming units per 100 mL. This concentration is developed by diluting the daily mass load of fecal coliform uniformly into the daily gross runoff and base flow. Although ten modeling years were completed, the 2005 recreational season is the only season provided on the figures.

Included on Figure C3 through C6, actual sampling results were provided from the 2005 filed survey of the Yellow Creek basin. For each HUC 14 modeled, the analytical results of fecal coliform compare to the after storm even t results of the BIT and SCS curve number method model. The model appears to be conservative in overestimating the upper bounds limit of fecal coliform during dry weather days. Thiess area weighted precipitation data is provided on each figure for the respective watershed.

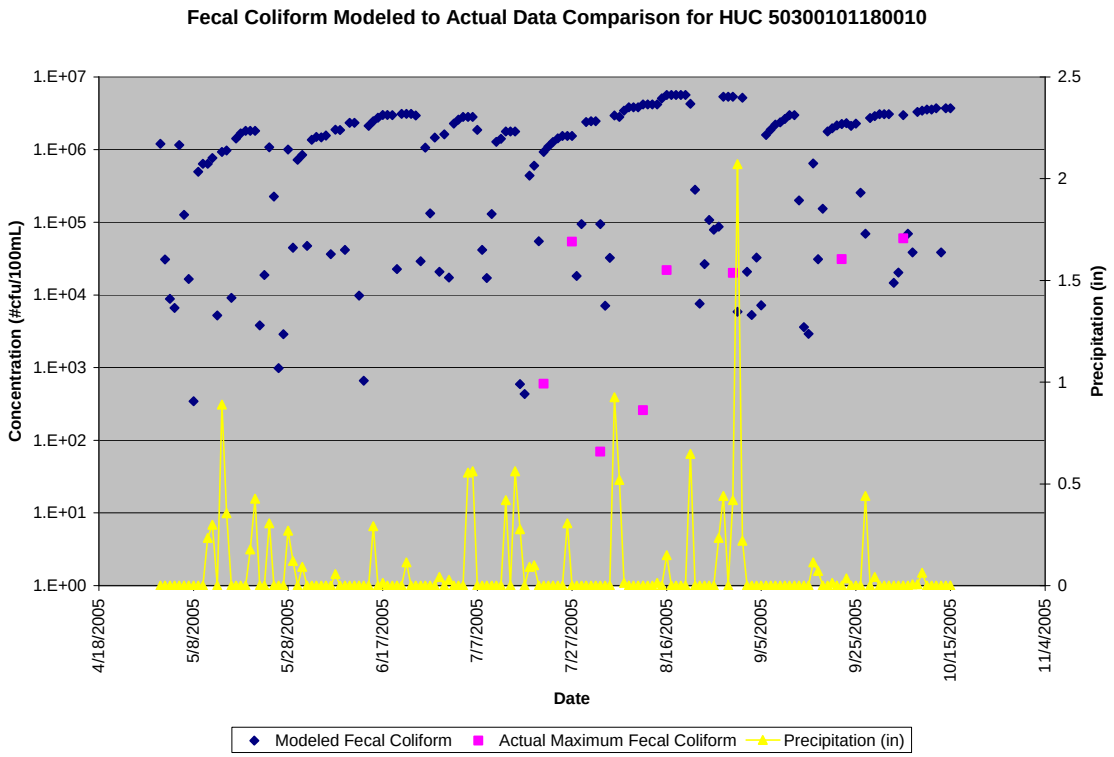

Figure C3. Modeled and actual fecal coliform concentrations for HUC 50300101-180-010 (2005)

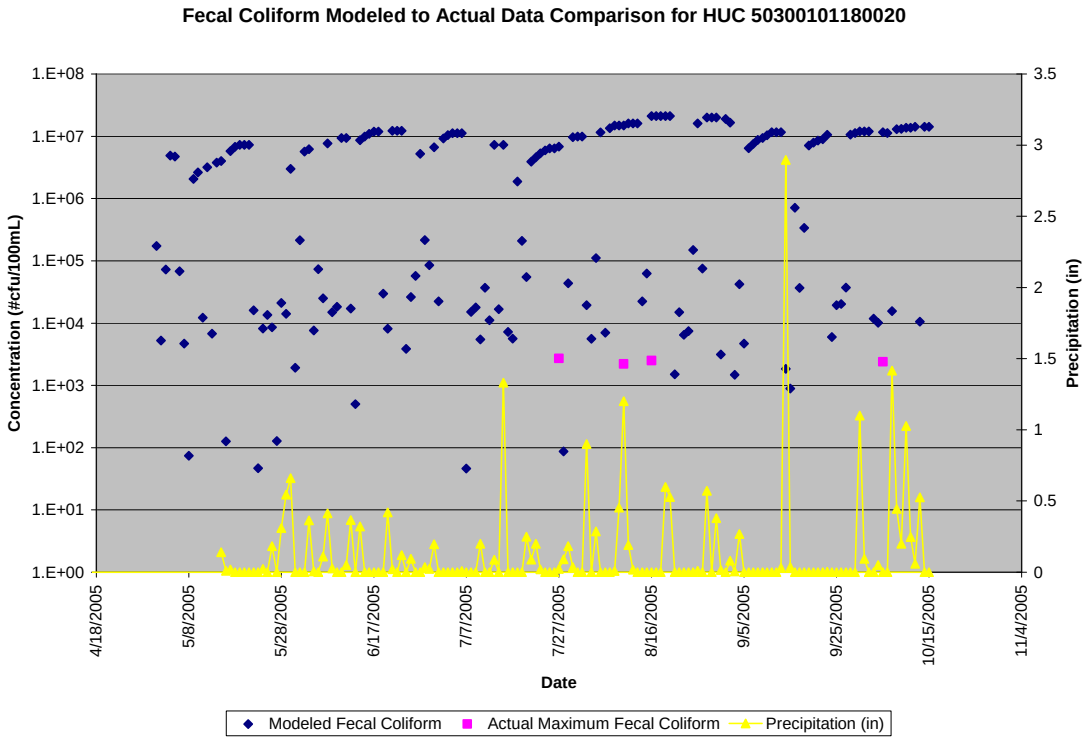

Figure C4. Modeled and actual fecal coliform concentrations for HUC 50300101-180-020 (2005)

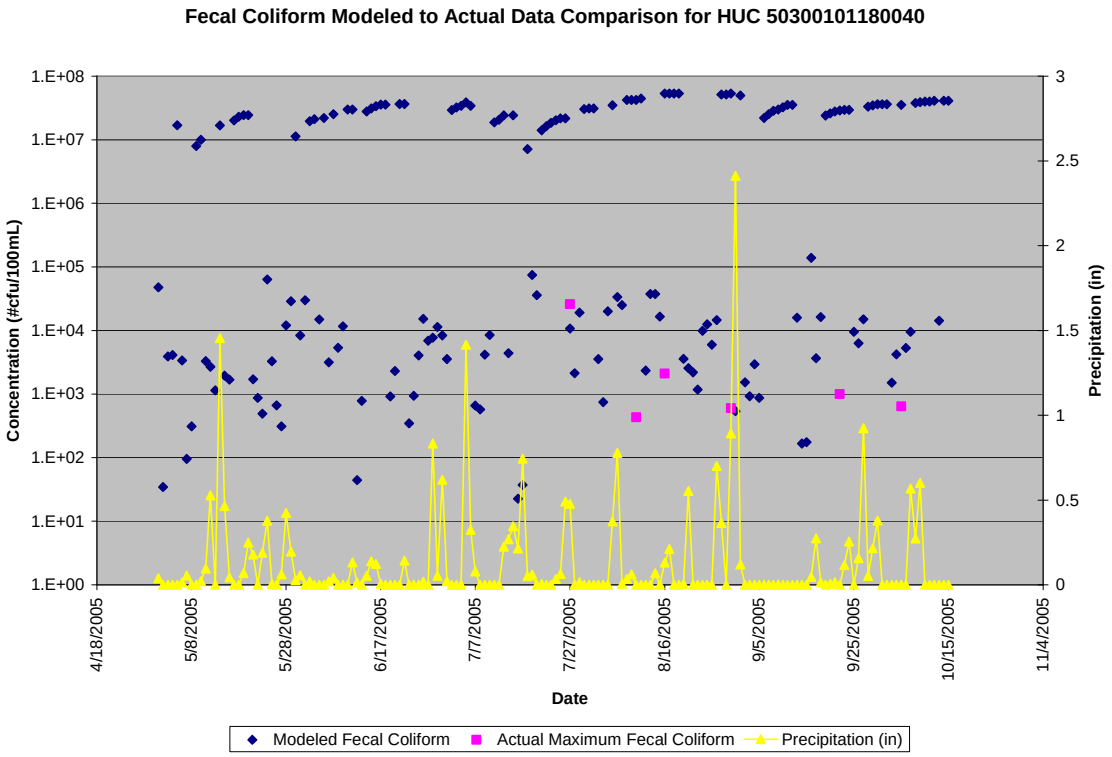

Figure C5. Modeled and actual fecal coliform concentrations for HUC 50300101-180-040 (2005)

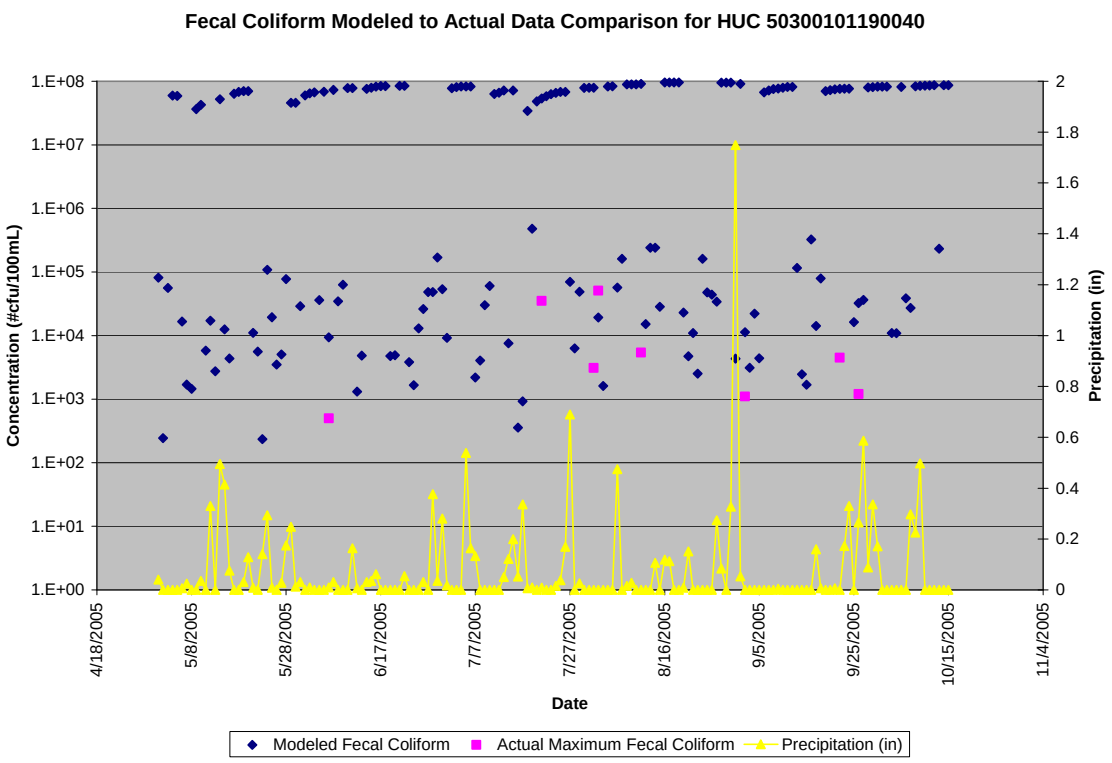

Figure C6. Modeled and actual fecal coliform concentrations for HUC 50300101-190-040 (2005)

Load Allocations

Load allocations were developed for nonpoint and point source loadings in support of the TMDL. These allocations lead to attainment of water quality standards. Allocation analysis was performed by applying the model to identify the assimilative capacity of the respective receiving water and determining how the allowable capacity can be allocated among the various sources. The allocations were developed by considering long term seasonal loadings of the daily geometric mean of 1000 coliform forming units per 100 milliliters of solution. The results of the allocations are presented in Table C5. The source loading reduction is proposed from repair and/or construction of onlot home sewage treatment systems as well as removal of direct animal inputs by eliminating grazing animals from entering the streams. Reductions of these two sources will be sufficient for the Yellow Creek watershed to meet Ohio's pathogen water quality standards.

Currently, a proposal to develop *E.* coli standards to replace the existing fecal coliform standards. Because Ohio EPA does not currently have the capability to model *E.* coli, an extensive comparison of the proportional values that occur in natural water for these two indicator type haves been completed on a state wide basis. Appendix D contains the fecal coliform, *E.* coli translator that was developed by Ohio EPA.

To compare the reduction percentages that are potentially affected by the proposed rule change, the fecal coliform data was translated utilizing the approved equation as follows:

$$E.\text{coli} = 0.403(\text{Fecal Coliform})^{1.028}$$

*E.*coli limits for primary contact recreational waters are currently proposed at a geometric mean standard of 206 cfu/100 mL. Reduction percentages to meet this standard for each of the HUC 14 drainage areas modeled is provided in Table C6. As can be determined from this table, the reduction percentages are significantly higher for *E.*coli than for the existing 1000 cfu/100 mL geometric mean standard for fecal coliform.

Table C5. Total Existing Bacteria Load, TMDL and Allocations for Yellow Creek (Total Fecal Coliform (#cfu) / average recreational season)

HUC 14	Total Loading		Margin of Safety	Major Source Allocations (#cfu/day)					Total Reduction (#cfu/day)
				Point Source	Septic	Agricultural Sources		Natural	
						Direct Animal Inputs	Overland Runoff		
5030101-180-010	Allowable	1.55E+16	5.0%	-	7.81E+15	7.61E+15	9.10E+13	1.42E+12	6.87E+16
	Existing	8.43E+16		-	7.66E+16	7.61E+15	9.10E+13	1.42E+12	
	% Reduction	81.6%		-	89.8%	0.0%	0.0%	0.0%	
5030101-180-020	Allowable	2.50E+16	5.0%	5.09E+12	1.46E+16	9.93E+15	4.53E+14	4.94E+12	4.76E+16
	Existing	7.26E+16		5.09E+12	6.22E+16	9.93E+15	4.53E+14	4.94E+12	
	% Reduction	65.5%		0%	76.5%	0.0%	0.0%	0.0%	
5030101-180-040	Allowable	4.76E+16	5.0%	-	4.11E+16	6.07E+15	4.23E+14	1.19E+13	2.04E+16
	Existing	6.80E+16		-	6.15E+16	6.07E+15	4.23E+14	1.19E+13	
	% Reduction	30.0%		-	33.1%	0.0%	0.0%	0.0%	
5030101-190-040	Allowable	9.28E+15	5.0%	1.50E+12	-1.24E+14	9.19E+15	2.19E+14	2.92E+12	7.58E+16
	Existing	8.51E+16		1.50E+12	7.57E+16	9.19E+15	2.19E+14	2.92E+12	
	% Reduction	89.1%		0%	100.0%	0.0%	0.0%	0.0%	

Table C6. Comparison of Fecal Coliform and E. coli reduction percentages for Yellow Creek for recreational attainment utilizing Ohio EPA fecal translator

			Recreational Season Bacteria Load by HUC 14			
	Sesonal Limit (CFU/100mL)	Parameter Comparison	05030101-180-010	05030101-180-020	05030101-180-040	05030101-190-040
Fecal Coliform	1000	Existing[1]	8.43E+16	7.26E+16	6.80E+16	8.51E+16
		TMDL[2]	1.63E+16	2.63E+16	5.01E+16	9.77E+15
		Exceedance	6.80E+16	4.63E+16	1.79E+16	7.53E+16
		% Reduction	80.6%	63.7%	26.3%	88.5%
E. coli	206	Existing[3]	1.18E+18	1.0E+18	9.5E+17	1.2E+18
		TMDL[4]	3.70E+16	5.97E+16	1.14E+17	2.21E+16
		Exceedance	1.14E+18	9.50E+17	8.34E+17	1.17E+18
		% Reduction	96.9%	94.1%	88.0%	98.1%

[1] Daily modeling utilized to develop mean seasonal load over 10 recreational seasons
[2] Fecal Coliform TMDL calculated at 1000 cfu/100 mL (geometric mean primary contact WQS)
[3] *E*.coli = 0.403(Fecal Coliform)$^{1.028}$
[4] *E*.coli TMDL calculated at 206 cfu/100 mL (Ohio EPA proposed geometric mean primary contact WQS)

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